

SEQUENCE LISTING

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Institute National de la Recherche Agronomique

<120> YEAST STRAINS WITH IMPROVED FRUCTOSE FERMENTATION CAPACITY

<130> 21568WO

<150> EP 03078992.9
<151> 2003-12-19

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<170> PatentIn version 3.1

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 <213> *Saccharomyces cerevisiae*

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aagaaaatgt tcggcaagaa ataa 1704

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<210> 26
<211> 567
<212> PRT
<213> Saccharomyces cerevisiae

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<400> 26

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          20           25           30

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Glu Glu Lys Gly Val Gln Asp Asp Phe Gln Ala Glu Ala Asp Gln Val
          35           40           45

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Leu Thr Asn Pro Asn Thr Gly Lys Gly Ala Tyr Val Thr Val Ser Ile
          50           55           60

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Cys Cys Val Met Val Ala Phe Gly Gly Phe Val Phe Gly Trp Asp Thr
65           70           75           80

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Gly Thr Ile Ser Gly Phe Val Ala Gln Thr Asp Phe Leu Arg Arg Phe
          85           90           95

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Gly Met Lys His Lys Asp Gly Ser Tyr Tyr Leu Ser Lys Val Arg Thr
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Gly Leu Ile Val Ser Ile Phe Asn Ile Gly Cys Ala Ile Gly Gly Ile
 115 120 125

Ile Leu Ala Lys Leu Gly Asp Met Tyr Gly Arg Lys Met Gly Leu Ile
 130 135 140

Val Val Val Val Ile Tyr Ile Ile Gly Ile Ile Ile Gln Ile Ala Ser
 145 150 155 160

Ile Asn Lys Trp Tyr Gln Tyr Phe Ile Gly Arg Ile Ile Ser Gly Leu
 165 170 175

Gly Val Gly Gly Ile Ala Val Leu Ser Pro Met Leu Ile Ser Glu Val
 180 185 190

Ala Pro Lys Glu Met Arg Gly Thr Leu Val Ser Cys Tyr Gln Leu Met
 195 200 205

Ile Thr Leu Gly Ile Phe Leu Gly Tyr Cys Thr Asn Phe Gly Thr Lys
 210 215 220

Asn Tyr Ser Asn Ser Val Gln Trp Arg Val Pro Leu Gly Leu Cys Phe
 225 230 235 240

Ala Trp Ala Leu Phe Met Ile Gly Gly Met Thr Phe Val Pro Glu Ser
 245 250 255

Pro Arg Tyr Leu Val Glu Ala Gly Gln Ile Asp Glu Ala Arg Ala Ser
 260 265 270

Leu Ser Lys Val Asn Lys Val Ala Pro Asp His Pro Phe Ile Gln Gln
 275 280 285

Glu Leu Glu Val Ile Glu Ala Ser Val Glu Glu Ala Arg Ala Ala Gly
 290 295 300

Ser Ala Ser Trp Gly Glu Leu Phe Thr Gly Lys Pro Ala Met Phe Lys
 305 310 315 320

Arg Thr Met Met Gly Ile Met Ile Gln Ser Leu Gln Gln Leu Thr Gly
 325 330 335

Asp Asn Tyr Phe Phe Tyr Tyr Gly Thr Thr Val Phe Asn Ala Val Gly

340	345	350
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370	375	380
Asn Cys Leu Leu Tyr Gly Ala Ile Gly Met Val Cys Cys Tyr Val Val		
385	390	395
Tyr Ala Ser Val Gly Val Thr Arg Leu Trp Pro Asn Gly Glu Gly Asn		
405	410	415
Gly Ser Ser Lys Gly Ala Gly Asn Cys Met Ile Val Phe Ala Cys Phe		
420	425	430
Tyr Ile Phe Cys Phe Ala Thr Thr Trp Ala Pro Ile Ala Tyr Val Val		
435	440	445
Ile Ser Glu Thr Phe Pro Leu Arg Val Lys Ser Lys Ala Met Ser Ile		
450	455	460
Ala Thr Ala Ala Asn Trp Leu Trp Gly Phe Leu Ile Gly Phe Phe Thr		
465	470	475
Pro Phe Ile Thr Gly Ala Ile Asn Phe Tyr Tyr Gly Tyr Val Phe Met		
485	490	495
Gly Cys Met Val Phe Ala Tyr Phe Tyr Val Phe Phe Phe Val Pro Glu		
500	505	510
Thr Lys Gly Leu Thr Leu Glu Glu Val Asn Asp Met Tyr Ala Glu Gly		
515	520	525
Val Leu Pro Trp Lys Ser Ala Ser Trp Val Pro Thr Ser Gln Arg Gly		
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Ala Asn Tyr Asp Ala Asp Ala Leu Met His Asp Asp Gln Pro Phe Tyr		
545	550	555
Lys Lys Met Phe Gly Lys Lys		
565		

<210> 27
 <211> 567
 <212> PRT
 <213> Mutated HXT3 protein
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Glu Glu Lys Gly Val Gln Asp Asp Phe Gln Ala Glu Ala Asp Gln Val
 35 40 45

Leu Thr Asn Pro Asn Thr Gly Lys Gly Ala Tyr Val Thr Val Ser Ile
 50 55 60

Cys Cys Val Met Val Ala Phe Gly Gly Phe Val Phe Gly Trp Asp Thr
 65 70 75 80

Gly Thr Ile Ser Gly Phe Val Ala Gln Thr Asp Phe Leu Arg Arg Phe
 85 90 95

Gly Met Lys His Lys Asp Gly Ser Tyr Tyr Leu Ser Lys Val Arg Thr
 100 105 110

Gly Leu Ile Val Ser Ile Phe Asn Ile Gly Cys Ala Ile Gly Gly Ile
 115 120 125

Ile Leu Ala Lys Leu Gly Asp Met Tyr Gly Arg Lys Met Gly Leu Ile
 130 135 140

Val Val Val Val Ile Tyr Ile Ile Gly Ile Ile Ile Gln Ile Ala Ser
 145 150 155 160

Ile Asn Lys Trp Tyr Gln Tyr Phe Ile Gly Arg Ile Ile Ser Gly Leu
 165 170 175

Gly Val Gly Gly Ile Ala Val Leu Ser Pro Met Leu Ile Ser Glu Val
 180 185 190

Ala Pro Lys Glu Met Arg Gly Thr Leu Val Ser Cys Tyr Gln Leu Met
 195 200 205

Val Thr Leu Gly Ile Phe Leu Gly Tyr Cys Thr Asn Phe Gly Thr Lys
 210 215 220

Asn Tyr Ser Asn Ser Val Gln Trp Arg Val Pro Leu Gly Leu Cys Phe
 225 230 235 240

Ala Trp Ala Leu Phe Met Ile Gly Gly Met Thr Phe Val Pro Glu Ser
 245 250 255

Pro Arg Tyr Leu Val Glu Ala Gly Gln Ile Asp Glu Ala Arg Ala Ser
 260 265 270

Leu Ser Lys Val Asn Lys Val Ala Pro Asp His Pro Phe Ile Gln Gln
 275 280 285

Glu Leu Glu Val Ile Glu Ala Ser Val Glu Glu Ala Arg Ala Ala Gly
 290 295 300

Ser Ala Ser Trp Gly Glu Leu Phe Thr Gly Lys Pro Ala Met Phe Lys
 305 310 315 320

Arg Thr Met Met Gly Ile Met Ile Gln Ser Leu Gln Gln Leu Thr Gly
 325 330 335

Asp Asn Tyr Phe Phe Tyr Tyr Gly Thr Thr Val Phe Asn Ala Val Gly
 340 345 350

Met Ser Asp Ser Phe Glu Thr Ser Ile Val Phe Gly Val Val Asn Phe
 355 360 365

Phe Ser Thr Cys Cys Ser Leu Tyr Thr Val Asp Arg Phe Gly Arg Arg
 370 375 380

Asn Cys Leu Leu Tyr Gly Ala Ile Gly Met Val Cys Cys Tyr Val Val
 385 390 395 400

Tyr Ala Ser Val Gly Val Thr Arg Leu Trp Pro Asn Gly Glu Gly Asn
 405 410 415

Gly Ser Ser Lys Gly Ala Gly Asn Cys Met Ile Val Phe Ala Cys Phe

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 Tyr Ile Phe Cys Phe Ala Thr Thr Trp Ala Pro Ile Ala Tyr Val Val
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 Ile Ser Glu Thr Phe Pro Leu Arg Val Lys Ser Lys Ala Met Ser Ile
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 Ala Thr Ala Ala Asn Trp Leu Trp Gly Phe Leu Ile Gly Phe Phe Thr
 465 470 475 480
 Pro Phe Ile Thr Gly Ala Ile Asn Phe Tyr Tyr Gly Tyr Val Phe Met
 485 490 495
 Gly Cys Met Val Phe Ala Tyr Phe Tyr Val Phe Phe Phe Val Pro Glu
 500 505 510
 Thr Lys Gly Leu Thr Leu Glu Glu Val Asn Asp Met Tyr Ala Glu Gly
 515 520 525
 Val Leu Pro Trp Lys Ser Ala Ser Trp Val Pro Thr Ser Gln Arg Gly
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 Lys Lys Met Phe Gly Lys Lys
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<210> 28
 <211> 1704
 <212> DNA
 <213> Mutated HXT3 gene

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aagaaaatgt tcggcaagaa ataa 1704

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<210> 29
<211> 1704
<212> DNA
<213> Mutated HXT3 gene II

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<210> 30

<211> 567

<212> PRT

<213> Mutated HXT3 protein II

<400> 30

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 20 25 30

Glu Glu Lys Gly Val Gln Asp Asp Phe Gln Ala Glu Ala Asp Gln Val
 35 40 45

Leu Thr Asn Pro Asn Thr Gly Lys Gly Ala Tyr Val Thr Val Ser Ile
 50 55 60

Cys Cys Val Met Val Ala Phe Gly Gly Phe Val Phe Gly Trp Asp Thr
 65 70 75 80

Gly Thr Ile Ser Gly Phe Val Ala Gln Thr Asp Phe Leu Arg Arg Phe
 85 90 95

Gly Met Lys His Lys Asp Gly Ser Tyr Tyr Leu Ser Lys Val Arg Thr
 100 105 110

Gly Leu Ile Val Ser Ile Phe Asn Ile Gly Cys Ala Ile Gly Gly Ile
 115 120 125

Ile Leu Ala Lys Leu Gly Asp Met Tyr Gly Arg Lys Met Gly Leu Ile
 130 135 140

Val Val Val Val Ile Tyr Ile Ile Gly Ile Ile Ile Gln Ile Ala Ser
 145 150 155 160

Ile Asn Lys Trp Tyr Gln Tyr Phe Ile Gly Arg Ile Ile Ser Gly Leu
 165 170 175

Gly Val Gly Gly Ile Ala Val Leu Ser Pro Met Leu Ile Ser Glu Val
 180 185 190

Ala Pro Lys Glu Met Arg Gly Ala Leu Val Ser Cys Tyr Gln Leu Met
 195 200 205

Val Thr Leu Gly Ile Phe Leu Gly Tyr Cys Thr Asn Phe Gly Thr Lys
 210 215 220

Asn Tyr Ser Asn Ser Val Gln Trp Arg Val Pro Leu Gly Leu Cys Phe
 225 230 235 240

Ala Trp Ala Leu Phe Met Ile Gly Gly Met Thr Phe Val Pro Glu Ser
 245 250 255

Pro Arg Tyr Leu Val Glu Ala Gly Gln Ile Asp Glu Ala Arg Ala Ser
 260 265 270

Leu Ser Lys Val Asn Lys Val Ala Pro Asp His Pro Phe Ile Gln Gln
 275 280 285

Glu Leu Glu Val Ile Glu Ala Ser Val Glu Glu Ala Arg Ala Ala Gly
 290 295 300

Ser Ala Ser Trp Gly Glu Leu Phe Thr Gly Lys Pro Ala Met Phe Lys
 305 310 315 320

Arg Thr Met Ile Gly Ile Met Ile Gln Ser Leu Gln Gln Leu Thr Gly
 325 330 335

Asp Asn Tyr Phe Phe Tyr Tyr Gly Thr Thr Val Phe Asn Ala Val Gly
 340 345 350

Met Ser Asp Ser Phe Glu Thr Ser Ile Val Phe Gly Val Val Asn Phe
 355 360 365

Phe Ser Thr Cys Cys Ser Leu Tyr Thr Val Asp Arg Phe Gly Arg Arg
 370 375 380

Asn Cys Leu Met Trp Gly Ala Val Gly Met Val Cys Cys Tyr Val Val
 385 390 395 400

Tyr Ala Ser Val Gly Val Thr Arg Leu Trp Pro Asn Gly Gln Asn Asn
 405 410 415

Gly Ser Ser Lys Gly Ala Gly Asn Cys Met Ile Val Phe Ala Cys Phe
 420 425 430

Tyr Ile Phe Cys Phe Ala Thr Thr Trp Ala Pro Ile Ala Tyr Val Val

435

440

445

Val Ser Glu Thr Phe Pro Leu Arg Val Lys Ser Lys Ala Met Ser Ile
 450 455 460

Ala Thr Ala Ala Asn Trp Ile Trp Gly Phe Leu Ile Gly Phe Phe Thr
 465 470 475 480

Pro Phe Ile Thr Gly Ala Ile Asn Phe Tyr Tyr Gly Tyr Val Phe Met
 485 490 495

Gly Cys Met Val Phe Ala Tyr Phe Tyr Val Phe Phe Phe Val Pro Glu
 500 505 510

Thr Lys Gly Leu Thr Leu Glu Glu Val Asn Asp Met Tyr Ala Glu Gly
 515 520 525

Val Leu Pro Trp Lys Ser Ala Ser Trp Val Pro Thr Ser Gln Arg Gly
 530 535 540

Ala Asn Tyr Asp Ala Asp Ala Leu Met His Asp Asp Gln Pro Phe Tyr
 545 550 555 560

Lys Lys Met Phe Gly Lys Lys
 565